



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/763,976  
Source: 1FWO  
Date Processed by STIC: 7/12/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

~~TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER~~  
~~VERSION 4.2 PROGRAM~~ ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/efb/efs/downloads/documents.htm>) , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box-1450, Alexandria, VA 22313-1450
3. Hand-Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):  
U.S. Patent and Trademark Office, 220 20<sup>th</sup> Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

## Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: <u>10/763,976</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input checked="" type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use <b>space characters</b> , instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n/Xaa	"n" can only represent a single <u>nucleotide</u> ; "Xaa" can only represent a single <u>amino acid</u>	



IFWO

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/763,976

DATE: 07/12/2004

TIME: 15:16:58

Input Set : N:\FATIMA\10763976.txt

Output Set: N:\CRF4\07122004\J763976.raw

3 <110> APPLICANT: Harms, Jerome S.  
 4 Splitter, Gary A.  
 5 Eakle, Kurt A.  
 6 Bremel, Robert D.  
 8 <120> TITLE OF INVENTION: Inducible Protein Expression System  
 W--> 0 <130> FILE REFERENCE:  
 10 <140> CURRENT APPLICATION NUMBER: US 10/763,976  
 C--> 11 <141> CURRENT FILING DATE: 2004-07-07  
 13 <160> NUMBER OF SEQ ID NOS: 13

*pp 1-4*

## ERRORED SEQUENCES

Does Not Comply  
 Corrected Diskette Needed

457 <210> SEQ ID NO: 7  
 458 <211> LENGTH: 309  
 459 <212> TYPE: PRT  
 460 <213> ORGANISM: bovine leukemia virus  
 462 <400> SEQUENCE: 7  
 464 Met Ala Ser Val Val Gly Trp Gly Pro His Ser Leu His Ala Cys  
 E--> 465 1     5     10     5     15     10     15  
 467 Pro Ala Leu Val Leu Ser Asn Asp Val Thr Ile Asp Ala Trp Cys  
 E--> 468     20     25     30  
 470 Pro Leu Cys Gly Pro His Glu Arg Leu Gln Phe Glu Arg Ile Asp  
 E--> 471     35     40     45  
 473 Thr Thr His Thr Cys Glu Thr His Arg Ile Thr Trp Thr Ala Asp  
 E--> 474     50     55     60  
 476 Gly Arg Pro Phe Gly Leu Asn Gly Ala Leu Phe Pro Arg Leu His  
 E--> 477     65     70     75  
 479 Val Ser Arg Asp Pro Ala Pro Arg Ala Arg Arg Leu Trp Ile Asn  
 E--> 480     80     85     90  
 482 Cys Pro Leu Pro Ala Val Arg Ala Gln Pro Gly Pro Val Ser Leu  
 E--> 483     95     100     105  
 485 Ser Pro Phe Glu Arg Ser Pro Phe Gln Pro Tyr Gln Cys Gln Leu  
 E--> 486     110     115     120  
 488 Pro Ser Ala Ser Ser Asp Gly Cys Pro Val Ile Gly His Gly Leu  
 E--> 489     125     130     135  
 491 Leu Pro Trp Asn Asn Leu Val Thr His Pro Cys Pro Arg Lys Val  
 E--> 492     140     145     150  
 494 Leu Ile Leu Asn Gln Met Ala Asn Phe Ser Leu Leu Pro Pro Phe  
 E--> 495     155     160     165  
 497 Asn Thr Leu Leu Val Asp Pro Leu Arg Leu Ser Val Phe Ala Pro  
 E--> 498     170     175     180  
 500 Asp Thr Arg Gly Ala Ile Arg Tyr Leu Ser Thr Leu Leu Thr Leu

*see p. 2*

*misaligned  
 amino acid  
 numbers  
 (see item 3 on  
 Error summary  
 sheet)*

## RAW SEQUENCE LISTING

DATE: 07/12/2004

PATENT APPLICATION: US/10/763,976

TIME: 15:16:58

Input Set : N:\FATIMA\10763976.txt

Output Set: N:\CRF4\07122004\J763976.raw

```

E--> 501      185   190   195
503 Cys Pro Ala Thr Cys Ile Leu Pro Leu Gly Glu Pro Phe Ser Pro
E--> 504      200   205   210
506 Asn Val Pro Ile Cys Arg Phe Pro Arg Asp Ser Asn Glu Pro Pro
E--> 507      215   220   225
509 Leu Ser Glu Phe Glu Leu Pro Leu Ile Gln Thr Pro Gly Leu Ser
E--> 510      230   235   240
512 Trp Ser Val Pro Ala Ile Asp Leu Phe Leu Thr Gly Pro Pro Ser
E--> 513      245   250   255
515 Pro Cys Asp Arg Leu His Val Trp Ser Ser Pro Gln Ala Leu Gln
E--> 516      260   265   270
518 Arg Phe Leu His Asp Pro Thr Leu Thr Trp Ser Glu Leu Val Ala
E--> 519      275   280   285
521 Ser Arg Lys Leu Arg Leu Asp Ser Pro Leu Lys Leu Gln Leu Leu
E--> 522      290   295   300
E--> 524 Glu Asn Glu Trp Leu Ser Arg Leu Phe (***) delete
E--> 525      305
571 <210> SEQ ID NO: 8
572 <211> LENGTH: 353
573 <212> TYPE: PRT
574 <213> ORGANISM: human T-lymphotropic virus 1
576 <400> SEQUENCE: 8
579 Met Ala His Phe Pro Gly Phe Gly Gln Ser Leu Leu Phe Gly Tyr
E--> 580 1      5    10    15
582 Pro Val Tyr Val Phe Gly Asp Cys Val Gln Gly Asp Trp Cys Pro
E--> 583      20    25    30
585 Ile Ser Gly Gly Leu Cys Ser Ala Arg Leu His Arg His Ala Leu
E--> 586      35    40    45
588 Leu Ala Thr Cys Pro Glu His Gln Ile Thr Trp Asp Pro Ile Asp
E--> 589      50    55    60
591 Gly Arg Val Ile Gly Ser Ala Leu Gln Phe Leu Ile Pro Arg Leu
E--> 592      65    70    75
594 Pro Ser Phe Pro Thr Gln Arg Thr Ser Lys Thr Leu Lys Val Leu
E--> 595      80    85    90
597 Thr Pro Pro Ile Thr His Thr Thr Pro Asn Ile Pro Pro Ser Phe
E--> 598      95   100   105
600 Leu Gln Ala Met Arg Lys Tyr Ser Pro Phe Arg Asn Gly Tyr Met
E--> 601     110   115   120
603 Glu Pro Thr Leu Gly Gln His Leu Pro Thr Leu Ser Phe Pro Asp
E--> 604     125   130   135
606 Pro Gly Leu Arg Pro Gln Asn Leu Tyr Thr Leu Trp Gly Gly Ser
E--> 607     140   145   150
609 Val Val Cys Met Tyr Leu Tyr Gln Leu Ser Pro Pro Ile Thr Trp
E--> 610     155   160   165
612 Pro Leu Leu Pro His Val Ile Phe Cys His Pro Gly Gln Leu Gly
E--> 613     170   175   180
615 Ala Phe Leu Thr Asn Val Pro Tyr Lys Arg Ile Glu Glu Leu Leu
E--> 616     185   190   195
618 Tyr Lys Ile Ser Leu Thr Thr Gly Ala Leu Ile Ile Leu Pro Glu

```

same  
This misalignment  
also occurs  
in sequences 2, 3,  
and 6

misaligned  
amino acid numbers

see p.3

## RAW SEQUENCE LISTING

DATE: 07/12/2004

PATENT APPLICATION: US/10/763,976

TIME: 15:16:58

Input Set : N:\FATIMA\10763976.txt

Output Set: N:\CRF4\07122004\J763976.raw

E--> 619      200      205      210  
 621 Asp Cys Leu Pro Thr Thr Leu Phe Gln Pro Val Arg Ala Pro Val  
 E--> 622      215      220      225  
 624 Thr Leu Thr Ala Trp Gln Asn Gly Leu Leu Pro Phe His Ser Thr  
 E--> 625      230      235      240  
 627 Leu Thr Thr Pro Gly Leu Ile Trp Thr Phe Thr Asp Gly Thr Pro  
 E--> 628      245      250      255  
 630 Met Ile Ser Gly Pro Cys Pro Lys Asp Gly Gln Pro Ser Leu Val  
 E--> 631      260      265      270  
 633 Leu Gln Ser Ser Ser Phe Ile Phe His Lys Phe Gln Thr Lys Ala  
 E--> 634      275      280      285  
 636 Tyr His Pro Ser Phe Leu Leu Ser His Gly Leu Ile Gln Tyr Ser  
 E--> 637      290      295      300  
 639 Ser Phe His Asn Leu His Leu Leu Phe Glu Glu Tyr Thr Asn Ile  
 E--> 640      305      310      315  
 642 Pro Ile Ser Leu Leu Phe Asn Lys Lys Glu Ala Asp Asp Asn Asp  
 E--> 643      320      325      330  
 645 His Glu Pro Gln Ile Ser Pro Gly Gly Leu Glu Pro Pro Ser Glu  
 E--> 646      335      340      345  
 E--> 648 Lys His Phe Arg Glu Thr Glu Val \*\*\*  
 E--> 649      350  
 685 <210> SEQ ID NO: 9  
 686 <211> LENGTH: 101  
 687 <212> TYPE: PRT  
 688 <213> ORGANISM: human immunodeficiency virus 1  
 690 <400> SEQUENCE: 9  
 692 Met Glu Pro Val Asp Pro Asn Leu Glu Pro Trp Lys His Pro Gly  
 E--> 693 1      5      10      15  
 695 Ser Gln Pro Arg Thr Ala Cys Asn Asn Cys Tyr Cys Lys Lys Cys  
 E--> 696      20      25      30  
 698 Cys Phe His Cys Tyr Ala Cys Phe Thr Arg Lys Gly Leu Gly Ile  
 E--> 699      35      40      45  
 701 Ser Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Ala Pro Gln  
 E--> 702      50      55      60  
 704 Asp Ser Gln Thr His Gln Ala Ser Leu Ser Lys Gln Pro Ala Ser  
 E--> 705      65      70      75  
 707 Gln Ser Arg Gly Asp Pro Thr Gly Pro Thr Glu Ser Lys Lys Lys  
 E--> 708      80      85      90  
 E--> 710 Val Glu Arg Glu Thr Glu Thr Asp Pro Phe Asp \*\*\*  
 E--> 711      95      100

*sane**sane**sane**see p. 4 for more error*

10/763,976 4

<210> 1  
<211> 576  
<212> DNA  
<213> Artificial Sequence

This needs explanation in <2207-2223> section.

<220>  
<221> Promoter  
<222> 87..432  
<223> BLV Promoter

Give source of  
genetic material.

<220>  
<221> misc\_feature  
<222> 452..576  
<223> attR1 Gateway recombination site  
  
<400> 1

IMPORTANT

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

Also, change all nucleotides from upper-case letters to lower-case letters

Since the Sequence Listing is in "new" Sequence Rules format, use lower-case letters for nucleotides.

**VERIFICATION SUMMARY**PATENT APPLICATION: **US/10/763,976**

DATE: 07/12/2004

TIME: 15:16:59

Input Set : **N:\FATIMA\10763976.txt**Output Set: **N:\CRF4\07122004\J763976.raw**

L:0 M:201 W: Mandatory field data missing, <130> FILE REFERENCE  
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:32 M:112 C: (48) String data converted to lower case,  
M:112 Repeated in SeqNo=1  
L:69 M:112 C: (48) String data converted to lower case,  
L:71 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
M:112 Repeated in SeqNo=2  
L:75 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:79 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:83 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:87 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:91 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:95 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:99 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:103 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:107 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:111 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:115 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:119 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:123 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:127 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:131 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:135 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:139 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:143 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:147 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:151 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:183 M:112 C: (48) String data converted to lower case,  
L:185 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
M:112 Repeated in SeqNo=3  
L:189 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:193 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:197 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:201 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:205 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:209 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:213 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:217 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:221 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:225 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:229 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:233 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:237 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:241 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:245 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:249 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:253 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:257 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/763,976

DATE: 07/12/2004

TIME: 15:16:59

Input Set : N:\FATIMA\10763976.txt

Output Set: N:\CRF4\07122004\J763976.raw

L:261 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
 L:265 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
 L:269 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
 L:273 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
 L:277 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
 L:297 M:112 C: (48) String data converted to lower case,  
 M:112 Repeated in SeqNo=4  
 L:354 M:112 C: (48) String data converted to lower case,  
 M:112 Repeated in SeqNo=5  
 L:411 M:112 C: (48) String data converted to lower case,  
 L:413 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6  
 M:112 Repeated in SeqNo=6  
 L:417 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6  
 L:421 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6  
 L:425 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6  
 L:429 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6  
 L:465 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7  
 M:332 Repeated in SeqNo=7  
 L:524 M:342 E: Invalid Stop Code On Error, STOP CODON: \*  
 L:525 M:252 E: No. of Seq. differs, <211> LENGTH:Input:309 Found:310 SEQ:7  
 L:580 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8  
 M:332 Repeated in SeqNo=8  
 M:342 Repeated in SeqNo=8  
 L:649 M:252 E: No. of Seq. differs, <211> LENGTH:Input:353 Found:354 SEQ:8  
 L:693 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9 ✓  
 M:332 Repeated in SeqNo=9  
 M:342 Repeated in SeqNo=9  
 L:711 M:252 E: No. of Seq. differs, <211> LENGTH:Input:101 Found:102 SEQ:9  
 L:795 M:112 C: (48) String data converted to lower case,  
 M:112 Repeated in SeqNo=10  
 L:1189 M:112 C: (48) String data converted to lower case,  
 M:112 Repeated in SeqNo=11  
 L:1530 M:112 C: (48) String data converted to lower case,  
 M:112 Repeated in SeqNo=12  
 L:1872 M:112 C: (48) String data converted to lower case,  
 M:112 Repeated in SeqNo=13